

ABSTRACT

The present invention provides methods for identifying polynucleotide and polypeptide sequences which may be associated with commercially or aesthetically relevant traits in domesticated plants or animals. The methods employ comparison of homologous genes from the domesticated organism and its ancestor to identify evolutionarily significant changes and evolutionarily neutral changes. Sequences thus identified may be useful in enhancing commercially or aesthetically desirable traits in domesticated organisms or their wild ancestors.

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